

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:03 ; Search time 221.672 Seconds
(without alignments)
10331.847 Million cell updates/sec

Title: US-09-807-933B-2

Perfect score: 1017
Sequence: 1 atgaagcttattactatgc.....caggtgttcagaataataa, 1017

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq, 101002.*

```
1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
```

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	100.0	1017	21	AAA62726
2	1017	100.0	1017	24	AAI43244
3	763	75.0	1101	21	AAA62727
4	763	75.0	1101	24	AAI43245
5	594.6	58.5	1043	21	AAA62732
6	594.6	58.5	1043	24	AAI43250
7	519.2	51.1	1083	21	AAA62728
8	519.2	51.1	1083	24	AAI43246
9	417.6	41.1	1017	21	AAA62729

10	417.6	41.1	1017	24	AAI43247
11	413	40.6	1164	21	AAA62730
12	413	40.6	1164	24	AAI43248
13	304.2	29.9	1041	21	AAA62731
14	304.2	29.9	1041	24	AAI43249
15	189.4	18.6	1473	12	AAQ14857
16	189.4	18.6	1473	13	AAQ26407
17	189.4	18.6	1473	13	AAQ26382
18	189.4	18.6	1473	13	AAQ25933
19	189.4	18.6	1473	13	AAQ29935
20	189.4	18.6	1473	14	AAQ49942
21	189.4	18.6	1473	16	AAZ60179
22	189.4	18.6	1473	19	AAV16103
23	187.8	18.5	1473	14	AAQ41733
24	185.2	18.2	984	19	AAV16105
25	181.2	17.8	927	17	AAV16062
26	181.2	17.8	1423	17	AAV19049
27	181	17.8	960	17	AAV19047
28	180.8	17.8	922	19	AAV15073
29	180	17.7	894	17	AAV19061
30	178.8	17.6	928	19	AAV15074
31	173.8	17.1	1132	17	AAV19053
32	169.6	16.7	922	19	AAV15072
33	165.4	16.3	1154	17	AAV19048
34	162.2	15.9	913	17	AAV19051
35	160.4	15.8	885	17	AAV19075
36	160	15.7	915	19	AAV15075
37	157.8	15.5	1261	19	AAV23748
38	154.8	15.2	925	19	AAV15076
39	153.6	15.1	1058	13	AAQ26405
40	153.6	15.1	1060	12	AAQ14856
41	153.6	15.1	1060	13	AAQ26380
42	153.6	15.1	1060	13	AAQ25932
43	153.6	15.1	1060	13	AAQ29934
44	153.6	15.1	1060	13	AAQ30072
45	153.6	15.1	1060	13	AAQ31181

ALIGNMENTS

RESULT 1
ID AAA62726 strand: DNA; 1017 BP.
AC AAA62726;
XX
DT 25-SEP-2000 (first entry)
XX
DE Endoglucanase nucleotide sequence 1.
XX
KW Endoglucanase; cellulose breakdown; produce pulp; papermaking;
KW animal foodstuff; ss.
XX
OS Rhizopus oryzae.
XX
PN WO200024879-A1.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-JP05884.
XX
PR 23-OCT-1998; 98JP-0302387.
XX
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
XX
PI Nakamura Y, Moriya T, Baba Y, Yanai K, Sumida N, Nishimura T;
PI Muraishima K, Nakane A, Yaguchi T, Koga J, Murakami T, Kono T;
XX
DR WPI, 2000-365117/31.
XX
DR P-PSDB; AAB09821.
XX
PT Endoglucanases of fungal origin with high activity under alkaline

conditions for production of paper pulp and animal feedstuffs
Claim 44; Page 104-105; 180pp; Japanese.

This sequence encodes an endoglucanase protein. The invention relates to an endoglucanase of fungal origin which can completely break down purified cellulose at a concentration of less than 1mg protein/litre, and produces more than 50% breakdown of cellulose at pH 8.5. The invention includes endoglucanase protein sequences (see AAB09825-B09830), endoglucanase nucleotide sequences (see AAB62726-A62732), and primers (AAB62733-A62802) which are used in the identification of the endoglucanase sequences, and in the construction of vectors containing the polynucleotides. The endoglucanase enzymes are used for the production of pulp for papermaking and for the production of animal feedstuffs.

Sequence 1017 BP; 240 A; 250 C; 235 G; 292 T; 0 other;

Query Match	100.0%	Score 1017;	DB 21;	Length 1017;
Best Local Similarity	100.0%;	Pred. No. 2.6e-299;		
Matches 1017; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	ATGAAAGTTATATACATTAATGAGCCCTTCGCGCTCTCTTGGCTCTCGCCCTCGGATCTGAAAG	60
Qy	1	ATGAAAGTTATATACATTAATGAGCCCTTCGCGCTCTCTTGGCTCTCGCCCTCGGATCTGAAAG	60
Db	1	ATGAAAGTTATATACATTAATGAGCCCTTCGCGCTCTCTTGGCTCTCGCCCTCGGATCTGAAAG	60
Qy	61	GGCTCGCTGCTGAAATGTAGCAAAATGTATGTCAATGTGTGTGTAAAGACTGAAATGGC	120
Qy	61	GGCTCGCTGCTGAAATGTAGCAAAATGTATGTCAATGTGTGTGTAAAGACTGAAATGGC	120
Db	61	GGCTCGCTGCTGAAATGTAGCAAAATGTATGTCAATGTGTGTGTAAAGACTGAAATGGC	120
Qy	121	CCTACTTGTGTGGAATCTGGAATCCACCCTGTGTAAGTAAGCAAGATTAATACTCTCAATGT	180
Qy	121	CCTACTTGTGTGGAATCTGGAATCCACCCTGTGTAAGTAAGCAAGATTAATACTCTCAATGT	180
Db	121	CCTACTTGTGTGGAATCTGGAATCCACCCTGTGTAAGTAAGCAAGATTAATACTCTCAATGT	180
Qy	181	CTTCCCTCTGGAAGCAGTGGCAATTAATCTTCTGAAAGTGCTCAAGAAAGATCACT	240
Qy	181	CTTCCCTCTGGAAGCAGTGGCAATTAATCTTCTGAAAGTGCTCAAGAAAGATCACT	240
Db	181	CTTCCCTCTGGAAGCAGTGGCAATTAATCTTCTGAAAGTGCTCAAGAAAGATCACT	240
Qy	241	GCTGCTCACAGAAGACTATCCGCTGCTCATATAAAAAGATCACTGCTCTGCTAAG	300
Qy	241	GCTGCTCACAGAAGACTATCCGCTGCTCATATAAAAAGATCACTGCTCTGCTAAG	300
Db	241	GCTGCTCACAGAAGACTATCCGCTGCTCATATAAAAAGATCACTGCTCTGCTAAG	300
Qy	301	AAGACTACAACTGTGTGCCAAGCTTCACCCCTCTAATCTACTCTAGCTCAAGGGC	360
Qy	301	AAGACTACAACTGTGTGCCAAGCTTCACCCCTCTAATCTACTCTAGCTCAAGGGC	360
Db	301	AAGACTACAACTGTGTGCCAAGCTTCACCCCTCTAATCTACTCTAGCTCAAGGGC	360
Qy	361	AAATATATCCGCTGCTCTGATGATGCTCTGTGGTAACGGTGTCACTACTGTATTTGGAT	420
Qy	361	AAATATATCCGCTGCTCTGATGATGCTCTGTGGTAACGGTGTCACTACTGTATTTGGAT	420
Db	361	AAATATATCCGCTGCTCTGATGATGCTCTGTGGTAACGGTGTCACTACTGTATTTGGAT	420
Qy	421	TGCTGTAAAGCCTCTGTAGACTGGCCCGGTAAAGCCAAATGTCACTTCTCTGTCAAGTCC	480
Qy	421	TGCTGTAAAGCCTCTGTAGACTGGCCCGGTAAAGCCAAATGTCACTTCTCTGTCAAGTCC	480
Db	421	TGCTGTAAAGCCTCTGTAGACTGGCCCGGTAAAGCCAAATGTCACTTCTCTGTCAAGTCC	480
Qy	481	TGTAAACAAGATGTGTCACTGCTCTTAAATGACACAAATGCCCAAAGTGCTGAACGT	540
Qy	481	TGTAAACAAGATGTGTCACTGCTCTTAAATGACACAAATGCCCAAAGTGCTGAACGT	540
Db	481	TGTAAACAAGATGTGTCACTGCTCTTAAATGACACAAATGCCCAAAGTGCTGAACGT	540
Qy	541	GGTAACAGTTACATGTGTAAACGACAACTTGGGCTGTAAACGACAACTTGCTAT	600
Qy	541	GGTAACAGTTACATGTGTAAACGACAACTTGGGCTGTAAACGACAACTTGCTAT	600
Db	541	GGTAACAGTTACATGTGTAAACGACAACTTGGGCTGTAAACGACAACTTGCTAT	600
Qy	601	GGTTCCGCTGCTGCGCATCAATGTGTGTGTGAATCTCGTGTGTGCTTTCTTTTTC	660
Qy	601	GGTTCCGCTGCTGCGCATCAATGTGTGTGTGTGAATCTCGTGTGTGCTTTCTTTTTC	660
Db	601	GGTTCCGCTGCTGCGCATCAATGTGTGTGTGTGAATCTCGTGTGTGCTTTCTTTTTC	660
Qy	661	GAACTTAATTTCACTTCACTTCTGTGTGCTGGTAAGAAATGTGTTCAGTCACTAAC	720
Qy	661	GAACTTAATTTCACTTCACTTCTGTGTGCTGGTAAGAAATGTGTTCAGTCACTAAC	720
Db	661	GAACTTAATTTCACTTCACTTCTGTGTGCTGGTAAGAAATGTGTTCAGTCACTAAC	720
Qy	721	ACTGTGTGTATCTTGGCTCTCTACATGGAGCTCACTTGAATTCAGAAATCCCGTGT	780
Qy	721	ACTGTGTGTATCTTGGCTCTCTACATGGAGCTCACTTGAATTCAGAAATCCCGTGT	780
Db	721	ACTGTGTGTATCTTGGCTCTCTACATGGAGCTCACTTGAATTCAGAAATCCCGTGT	780

QY	781	GGTGTGGATTTTCAAGGTTGTCACAGCCAAAGGGGTGCTCCCAATGACGGTTGGAGC	840
QY	781	GGTGTGGATTTTCAAGGTTGTCACAGCCAAAGGGGTGCTCCCAATGACGGTTGGAGC <td>840</td>	840
Db	781	GGTGTGGATTTTCAAGGTTGTCACAGCCAAAGGGGTGCTCCCAATGACGGTTGGAGC <td>840</td>	840
QY	841	TCAAGATACGGTGTATTTCTTCGCATCTGACGTGCTAGTCTTCTTCGCACTTCCA	900
Db	841	TCAAGATACGGTGTATTTCTTCGCATCTGACGTGCTAGTCTTCTTCGCACTTCCA	900
QY	901	GCTGGTTTGAATGAGATTCAACTGGTTCAAGAAAGCTGATTAACCCAGACATGACTTAC	960
Db	901	GCTGGTTTGAATGAGATTCAACTGGTTCAAGAAAGCTGATTAACCCAGACATGACTTAC	960
QY	961	AGGAGATTAACGTCCTCAGAGAAATCAACCGCAGACAGGTTGTTCAAGAAATAA	1017
Db	961	AGGAGATTAACGTCCTCAGAGAAATCAACCGCAGACAGGTTGTTCAAGAAATAA	1017

RESULT 2
AAL43244
ID AAL43244 standard; DNA; 1017 BP.

22-AUG-2002 (first entry)

Rhizopus arrhizus endoglucanase-related coding sequence 1.1

zygomycetes-originated endoglucanase; cellulose binding domain
fibre processing; waste paper de-inking; paper pulp; ds; gene.

Rhizopus arrhizus.

WO200242474-A1.

30-MAY-2002

21-NOV-2001; 2001WO-JP10188

21-NOV-2000; 2000JP-0354296.

(MEIJ) MEIJI SEIKA KAISHA LTD.

Nakane A, Baba Y, Koga J, Kubota H,

WPI; 2002-471729/50.

0
1
2
3
4
5
6

with effect of endoglucanase activity enhanced in processing fibers, achieving waste paper and improving freeness of paper pulp -

Example 10: Page 56-58: 109m: Japanese.

The invention comprises the amino acid

binding domain. The zygomycetes-origina-

The invention comprises the amino acid and coding sequences of xyloglucanase-originate endoglucanase enzymes lacking the cellulose binding domain. The xyloglucanase-originate endoglucanase enzymes of the invention have enhanced endoglucanase activity. The xyloglucanase-originate endoglucanase enzymes of the invention are useful for processing fibres, de-linking waste paper and improving the freeness of paper pulp - which is particularly applicable in detergent compositions. The present DNA sequence represents an endoglucanase-related gene sequence of the invention.

Sequence 1017 BP; 240 A; 250 C; 235 G; 292 T; 0 other/

Query Match	100.0%;	Score 1017;	DB 24;	Length 1017;
Best Local Similarity	100.0%;	Pred. No. 2.6e-299;		
Matches 1017;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ATGAAGTTATTACTATGTCCTCCCGCTCTTGGCTCTCGCCCTCGGTACTGTAATG 60
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 ATGAAGTTATTACTATGTCCTCCCGCTCTTGGCTCTCGCCCTCGGTACTGTAATG 60

OS Synthetic.
 XX PN WO200242474-A1.
 XX PD 30-MAY-2002.
 XX PF 21-NOV-2001; 2001WO-JP10188.
 XX PR 21-NOV-2000; 2000JP-0354296.
 XX PA (MEIJ) MEIJI SEIKA KAISHA LTD.
 XX PI Nakane A, Baba Y, Koga J, Kubota H;
 XX DR WPI; 2002-471729/50.
 XX DR P-PSDB; AAO15052.
 XX PT Cellulose-binding domain-lacking Zygomycetes-originated endoglucanase,
 XX PT with effect of endoglucanase activity enhanced in processing fibers,
 XX PT deinking waste paper and improving freeness of paper pulp -
 XX PS Example 10; Page 84-86; 109pp; Japanese.
 CC The invention comprises the amino acid and coding sequences of
 CC zygomycetes-originated endoglucanase enzymes lacking the cellulose
 CC binding domain. The zygomycetes-originated endoglucanase enzymes of the
 CC invention have enhanced endoglucanase activity. The zygomycetes-
 CC originated endoglucanase enzymes of the invention are useful for
 CC processing fibres, de-inking waste paper and improving the freeness of
 CC paper pulp - which is particularly applicable in detergent compositions.
 CC The present DNA sequence represents an endoglucanase-related gene
 CC sequence of the invention.
 SQ Sequence 1043 BP; 212 A; 370 C; 291 G; 170 T; 0 other;

Query Match 58.5%; Score 594.6; DB 24; Length 1043;
 Best Local Similarity 74.0%; Pred. No. 1,4e-170;
 Matches 753; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 1 ATGAAGTTTATTAATCTATGCTCTTCCGCTCTTGGCTCTCGGCTCGGTAAGTGAATG 60
 DB 16 ATGAAGTTTATTAATCTATGCTCTTCCGCTCTTGGCTCTCGGCTCGGTAAGTGAATG 75
 QY 61 GCCTTGGCTCTGTAATGTAAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 120
 DB 76 GCCTTGGCTCTGTAATGTAAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 135
 QY 121 CCTACTTGTGTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 180
 DB 136 CCTACTTGTGTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 195
 QY 181 CTTCCTCTGTAAGCAAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 240
 DB 196 CTTCCTCTGTAAGCAAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 255
 QY 241 GCTGCTCAAGAAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 300
 DB 256 GCTGCTCAAGAAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 315
 QY 301 AAGACTCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGT 360
 DB 316 AAGACTCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGT 375
 QY 361 AATATTTCCGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCT 420
 DB 376 AATATTTCCGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCT 435
 QY 421 TGTCTGAAGGCTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCT 480
 DB 436 TGTCTGAAGGCTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCT 495
 QY 481 TGTAAACAAGATGTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCTCTGCTGTCT 540

DB 496 TGCACAGAGACGGCTCAACCGCTTTAGGCACTCCAACGCCAGTCCGGCTGCAACGGC 555
 QY 541 GGTAAAGTTTAACTGTGTAAACGCAACCAACTTTGGGCTGTAAAGCAACCTTGCTTAT 600
 DB 556 GGTAAAGTTTAACTGTGTAAACGCAACCAACTTTGGGCTGTAAAGCAACCTTGCTTAT 615
 QY 601 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 616 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
 QY 661 GAACCTACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 720
 DB 676 GAACCTACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 735
 QY 721 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 DB 736 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
 QY 781 GGTGTTGTAATTTTCAATGTTGTTTCAAGCAATGAGGAGTCTTCCAAATGACGTTGGGGC 840
 DB 796 GGTGTTGTAATTTTCAATGTTGTTTCAAGCAATGAGGAGTCTTCCAAATGACGTTGGGGC 855
 QY 841 TCAAGATACGCTGTGTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB 856 TCAAGATACGCTGTGTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
 QY 901 GCTGTTGTAATTTTCAATGTTGTTTCAAGCAATGAGGAGTCTTCCAAATGACGTTGGGGC 960
 DB 916 GCTGTTGTAATTTTCAATGTTGTTTCAAGCAATGAGGAGTCTTCCAAATGACGTTGGGGC 975
 QY 961 AAGGAAGTTACTGCTCTTCAAGGAATTCACCGCCAGACAGTGTGTTCAAGAAATTA 1017
 DB 976 AAGGAAGTTACTGCTCTTCAAGGAATTCACCGCCAGACAGTGTGTTCAAGAAATTA 1032

RESULT 7
 AAA62728
 ID AAA62728 standard; DNA; 1083 BP.

XX AAA62728;

AC 25-SEP-2000 (first entry)

XX Endoglucanase nucleotide sequence 3.

DE Endoglucanase; cellulose breakdown; produce pulp; papermaking;

KW animal foodstuff; ss.

XX Rhizopus oryzae.

XX WO200024879-A1.

PN 04-MAY-2000.

PD 25-OCT-1999; 99WO-JP05884.

PF 23-OCT-1998; 98JP-0302387.

XX (MEIJ) MEIJI SEIKA KAISHA LTD.

PI Nakamura Y, Moriya T, Baba Y, Yanai K, Sumida N, Nishimura T;

PI Murashima K, Nakane A, Yaguchi T, Koga J, Murakami T, Kono T;

XX WPI; 2000-365117/31.

DR P-PSDB; AAB09823.

XX Endoglucanases of fungal origin with high activity under alkaline

PT conditions for production of paper pulp and animal feedstuffs -

PS Claim 44; Page 113-115; 180pp; Japanese.

CC This sequence encodes an endoglucanase protein. The invention relates

to an endoglucanase of fungal origin which can completely break down

CC purified cellulose at a concentration of less than 1mg protein/litre,
 CC and produces more than 50% breakdown of cellulose at pH 8.5. The
 CC invention includes endoglucanase protein sequences (see
 CC AAB09823-B09830), endoglucanase nucleotide sequences (see
 CC AAA62726-A62732) and primers (AAA62733-A62802) which are used in the
 CC identification of the endoglucanase sequences, and in the construction of
 CC vectors containing the polynucleotides. The endoglucanase enzymes are
 CC used for the production of pulp for papermaking and for the production of
 CC animal feedstuffs.

XX Sequence 1083 BP; 260 A; 297 C; 231 G; 295 T; 0 other;

Query Match 51.1%; Score 519.2; DB 21; Length 1083;

Best Local Similarity 71.9%; Pred. No. 1.4e-147; Indels 72; Gaps 5;

Matches 781; Conservative 0; Mismatches 233; Indels 72; Gaps 5;

QY 1 ATGAAGTTATTACTATGCTCTTCCGCTCTTGGCTCTCGCCCTCGGTACTGAAGT 60
 DB 1 ATGAAGTTCTTACCACTTGCTCTCGGCTCTTGGCACTTGGCACTTGGCACTTGAAGT 60
 QY 61 GCGCTGCTGCTGAATGTAAGCAATTTGTAAGTCAATGTAAGTGAAGTGAAGTGGC 120
 DB 61 GCGCAATGCTGCTGAAGTGAAGCAAGGCTTACTACCAATGTAAGTGAAGTGAAGTGA 120
 QY 121 CCTACTGTTGTAATCTGATCTGATCTG-----TAAAGTAAAGCAAGTACTACTCT 174
 DB 121 CCTACTGCTGTAATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 180
 QY 175 CAATGCTCTTCCCTGTAAGCAAGTGC-----TAAAGTAAAGCAAGTACTACTCT 210
 DB 181 CAATGCTCTTCCCAATGAAGCAAGTGC-----TAAAGTAAAGCAAGTACTACTCT 240
 QY 211 TGTGAAGTCTCAAGCAAGCAAGTACTACTGCTGCTCAAGCAAG--ACTACTACCGCT 267
 DB 241 ACTGAAGTGCCTCAAGCAAGCAAGTACTACTCAAGCAAGCAAGCAAGCAAGTACTGA 300
 QY 268 GCTCATAAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCC 327
 DB 301 GCTCTTAAGCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 360
 QY 328 A-----CCCTTCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 351
 DB 361 AAGAAAGCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 420
 QY 352 TCCAGCGGCAATATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
 DB 421 GCTTCTAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 480
 QY 412 TATTGGATGCTGTAAGGCTCTGTAAGGCTCTGTAAGGCTCTGTAAGGCTCTGTAAGGCTCT 471
 DB 481 TACTGGATGCTGTAAGGCTCTGTAAGGCTCTGTAAGGCTCTGTAAGGCTCTGTAAGGCTCT 540
 QY 472 GTCAGTCTCTGTAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 511
 DB 541 GTTGGCTCTGTAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 597
 QY 532 TGTAAAGTGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 591
 DB 598 TGTGGTGTGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 657
 QY 592 CTGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
 DB 658 CTGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
 QY 652 TCTTGTGCAACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 711
 DB 718 GCTGTTTGAACCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 777
 QY 712 GTTAACTCAAGT 771
 DB 778 GTTAACTCAAGT 837
 QY 772 CCGGCTGT 831

DB 838 CCGGCTGT 897
 QY 832 GCTTGGGCTCAAGTACGCTGTATTTCTTGTGATCTGATCTGATCTGATCTGATCTGATCT 891
 DB 898 GCTTGGGCTCAAGTACGCTGTATTTCTTGTGATCTGATCTGATCTGATCTGATCTGATCT 957
 QY 892 GCATCCAAAGCTGT 951
 DB 958 GCTTCAAGCTGT 1017
 QY 952 ATGACTTCAAGAAAGTACTGCTGCTTCAAGAAATCAAGCAAGCAAGCAAGCAAGCAAG 1011
 DB 1018 ATGACTTCAAGAAAGTACTGCTGCTTCAAGAAATCAAGCAAGCAAGCAAGCAAGCAAG 1077
 QY 1012 AAATAA 1017
 DB 1078 AAATAA 1083

RESULT 8
 ID AAL43246 standard; DNA; 1083 BP.

AC AAL43246;
 XX
 DT 22-AUG-2002 (first entry)

DE Rhizopus arrhizus endoglucanase-related coding sequence 3.

KW Zygomycetes-originated endoglucanase; cellulose binding domain;
 KM fibre processing; waste paper de-inking; paper pulp; db; gene.

OS Rhizopus arrhizus.

PN WO200242474-A1.

PD 30-MAY-2002.

PF 21-NOV-2001; 2001WO-JP10188.

PR 21-NOV-2000; 2000JP-0354296.

PA (MEIJ) MEIJ SEIKA KAISHA LTD.

PI Nakane A, Baba Y, Koga J, Kubota H;

PS WPI; 2002-471729/50.

DR P-PSDB; AAO15054.

PT Cellulose-binding domain-lacking Zygomycetes-originated endoglucanase,
 PT with effect of endoglucanase activity enhanced in processing fibers,
 PT deinking waste paper and improving freeness of paper pulp -

XX disclosure; Page 65-68; 109pp; Japanese.

CC The invention comprises the amino acid and coding sequences of
 CC zygomycetes-originated endoglucanase enzymes lacking the cellulose
 CC binding domain. The zygomycetes-originated endoglucanase enzymes of the
 CC invention have enhanced endoglucanase activity. The zygomycetes-
 CC originated endoglucanase enzymes of the invention are useful for
 CC processing fibres, de-inking waste paper and improving the freeness of
 CC paper pulp - which is particularly applicable in detergent compositions.
 CC The present DNA sequence represents an endoglucanase-related gene
 CC sequence of the invention.

XX Sequence 1083 BP; 260 A; 297 C; 231 G; 295 T; 0 other;

Query Match 51.1%; Score 519.2; DB 24; Length 1083;

Best Local Similarity 71.9%; Pred. No. 1.4e-147; Indels 72; Gaps 5;

Matches 781; Conservative 0; Mismatches 233; Indels 72; Gaps 5;

QY 1 ATGAAGTTATTACTATGCTCTTCCGCTCTTGGCTCTCGCCCTCGGTACTGAAGT 60

Db	1	ATGAAGTTCCTTACATTCGCTCCCTCCCGGTATCTTGCGACTTGCGCGTGGTACTGAATG	60
Qy	61	GCCTTCGCTGCTGAATGTGACAAATTGTAATGTGATCATGTGGTGTAAAGACTGGAATGCG	120
Db	61	GCCCAATGCTGCGAATGTGAGCAAGGCTTACTCAATGATGGGTGTAAAGACTGGATGGA	120
Qy	121	CCTACTTGTGTGATCTGATCCACCTG-----TAAAGTAAAGCAAGATTACTACTCT	174
Db	121	CCTACTCTGTGATCTGTGCTCTTACTTTCGTTATTAATCCGACAACTCTTCTTACTCTC	180
Qy	175	CAATGCTTTCCTCTGGAAGCAGTGGC-----ATAATATCT	210
Db	181	CAATGTGTTCCCAATGAAAACTCCACCTCCACTTAACAAATCTTCCACAAAACCAACT	240
Qy	211	TCTGAAAGGCTCACAGAAAGCTACCACTGCTGCTCCACAAAG---ACTATCAACGGT	267
Db	241	ACTGAGAGTCCAGAAAGCTACCACTTAAAGTTCCAAAGAACCACTACTCTGAA	300
Qy	268	GCTCAATAAAGACTACCACTGCTCCTGTGTAAGAAACTACAACTGTTGCCAAAGCTTCC	327
Db	301	GCTCTAAGAAAGACCACTACTGAAAGTTCCAAAGAACCACTACTGAAAGCTCT	360
Qy	328	A-----GCCCTTCACTTACTGCTCTACG	351
Db	361	AAGAAAGCACCACTACTAAGAAAGGCTTCTACTCTCCACTCTCTCTCTCTCTCTCT	420
Qy	352	TCCAGCGGCAATATATCCGCTGTCTGTGGTGGCTCTGGTAAAGGTCTCACTACTG	411
Db	421	GCTTCTACAACTACTCCGCTCTCTGTGGTGGCTCCGGTAAATGTGAACCACTCCG	480
Qy	412	TATTGGGATGCTGTAAAGGCTCTCGTAACTGAGCCCGGTAAAGGCCAATGTCAATTCTCT	471
Db	481	TACTGGGATGTGTAAAGCTTCTTGGCAAGTTGGCCCGGTAAAGCTGAATGTCACTCCCT	540
Qy	472	GTCAAGTCCCTGTAAACAAAGATGTGTCACTGCTTAAAGACAGCAATGCCAAAGTGGC	531
Db	541	GTTGGCTCCTGTAAACAAAGATGTGAAGTCT---CTTGTGTAAACAACTCAAAAGCGC	597
Qy	532	TGTAAAGGTGTAAAGATGTATGTGTAAAGCAACCAACTTGGGCTGTAAAGCAAC	591
Db	598	TGTGTGTGGGTAAAGAGCTACCACTGTAAATGAACAATCAACTTGGGTTGTAAAGCAAGC	657
Qy	592	CTTGGCTAATGTTTGGCTGCTGCTGCACTGAATGGTGGTGGATCTCCGTGGTGGT	651
Db	658	CTTGGCTAATGTTTGGCTGCTGCTGCACTGAATGGTGGTGGATCTCCGTGGTGGT	717
Qy	652	TCTTGTTCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	711
Db	718	GCTGTTCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	777
Qy	712	GTCACTAACAATGTGTGTATCTTGCTCTCTAATGTGTGTCACTTTGATCTTGAATG	771
Db	778	GTAAACAACAATGTGTGTATCTTGCTCTTAAACATGTGTGTCACTTTGATCTTGAATG	837
Qy	772	CCCGGTGGTGGTGTGTATTTTCAATGGTGTTCAGGCAATGGGGTCTCCCAATGAC	831
Db	838	CCCGGTGGTGGTGTGTATTTTCAATGGTGTTCAGGCAATGGGGTCTCCCAATGAC	897
Qy	832	GGTGGGGGCTCAAGATACGATGTATTTCTTGTCAATCTGACTGCTTACTGCTCTCC	891
Db	898	GGTGGGGGCTCAAGATACGATGTATTTCTTGTCAATCTGACTGCTTACTGCTCTCC	957
Qy	892	GCATCTCAAGCTGTGTAAATGTGAATCACTGTTTAAAGAACGTGTATTAACCAAGC	951
Db	958	GCCCTTCAAGCTGTGTGTAAATGTGAATCACTGTTTAAAGAACGTGTATTAACCAAGC	1011
Qy	952	ATGACTTAAACGAAGTACTCTGTCTTAAGAAATACCGCAAGACAGGTTGTTCAAGA	1011
Db	1018	ATGACTTAAACGAAGTACTCTGTCTTAAGAAATACCGCAAGACAGGTTGTTCAAGA	1077
Qy	1012	AAATAA	1017

Db	1078	AAATPA	1083
		RESULT 9	
		AAA62729	
Id		AAA62729	standard; DNA; 1017 BP.
XX		AAA62729;	
XX		25-SEP-2000	(first entry)
XX		Endoglucanase nucleotide sequence 4.	
XX		Endoglucanase; cellulose breakdown; produce pulp; papermaking;	
KW		animal foodstuff; ss.	
XX		Mucor circinelloides.	
OS		WO200024879-A1.	
XX		04-MAY-2000.	
PD		25-OCT-1999;	99WO-JP05884.
XX		23-OCT-1998;	98JP-0302387.
XX		(MEIJ) MEIJI SEIKA KAISHA LTD.	
PA		Nakamura Y, Moriya T, Baba Y, Yanai K, Sumida N, Nishimura T;	
PI		Murashima K, Nakane A, Yaguchi T, Koga J, Murakami T, Kono T;	
DR		WPI: 2000-365117/31.	
XX		P-PSDB; AAB09824.	
XX		Endoglucanases of fungal origin with high activity under alkaline	
PT		conditions for production of paper pulp and animal feedstuffs -	
PS		Claim 44; Page 118-119; 180pp; Japanese.	
XX		This sequence encodes an endoglucanase protein. The invention relates	
CC		to an endoglucanase of fungal origin which can completely break down	
CC		purified cellulose at a concentration of less than 1mg protein/1litre,	
CC		and produces more than 50% breakdown of cellulose at pH 8.5. The	
CC		invention includes endoglucanase protein sequences (see	
CC		AA093825-A093830), endoglucanase nucleotide sequences (see	
CC		AAA62726-A62732) and primers (AAA62733-A62802) which are used in the	
CC		identification of the endoglucanase sequences, and in the construction of	
CC		vectors containing the polynucleotides. The endoglucanase enzymes are	
CC		used for the production of pulp for papermaking and for the production of	
CC		animal foodstuffs.	
CC		Sequence 1017 BP; 233 A; 255 C; 236 G; 293 T; 0 other;	
SQL			
		Query Match	41.1%; Score 417.6; DB 21; Length 1017;
		Best Local Similarity	67.8%; Pred. No. 1.2e-116;
		Matches 655; Conservative	0; Mismatches 284; Indels 27; Gaps 4
QY		67	GCTGTTGAATGAGCAAAATTGATGTCATAATGTTGGTGAAGACGTAATGGCCCTACT 126
DB		64	GCTGTTCTTTGGAGCTCTGTCATGTCATGTCATGTTGGTGGATTGGATGGAGTGAACCTACC 123
QY		127	TGTTTGTAATCTGCATCCACCTG-----TAAAGTAGCAACGATTACTACTCTCAATGT 180
DB		124	TGTTTGAAAGTGGTCTACTACTTGCGTTGTGTCAAGAAAGGCAAAATVACTACTCTCAATGT 183
QY		181	CTTCCCTCTGGAAGCAGTGGCGCATTAATCTTTGAAAGTGCTCAAGAAGAC----- 233
DB		184	CTTCCCGGATCCACAGTAACTATCTGGTTAACGCTAGACGACCAAGAAAGCATCTACC 243
QY		234	--TACACATGCTGCTCACAAAGAACTACTACCGCTGCTCATATAAAAGACTACATGCT 291
DB		244	AAGACATCTACTACCAACCGCCACAGGCTACTGTACTCTGTACACCAAGACAGTAAACAAAG 303

```

OY 292 CCGGCTAAGAGACTACGATCTTGCCAAAGCTTCACCCCTTCTAAGCTCTAGCTCTAGC 351
DB 304 ACACTACCAAGACAATCAAGACTACGACCTGCGGCTTCTAAGCTCTAGCTCTAGC 363
OY 352 TCCAGCGGCAATATTCGCGCTGCTCTGAGTGTGCTCTGCTGCTGCTGCTGCTGCTGCT 411
DB 364 TCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
OY 412 TATTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
DB 424 TATTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
OY 472 GTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
DB 484 GTTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
OY 532 TGTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
DB 541 TGTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
OY 592 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
DB 601 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
OY 652 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 711
DB 661 GCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
OY 712 GTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
DB 721 GTTACCAACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
OY 772 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831
DB 772 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831
OY 832 GGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
DB 832 GGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
OY 892 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
DB 892 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
OY 952 ATGACTTCAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
DB 952 ATGACTTCAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
OY 1012 AATATA 1017
DB 1012 AATATA 1017

```

```

RESULT 10
AAL43247
AAL43247 standard; DNA; 1017 BP.
XX AAL43247;
XX
XX
XX 22-AUG-2002 (first entry)
XX
XX Rhizopus arrhizus endoglucanase-related coding sequence 4.
XX
XX Zymomyces-originated endoglucanase; cellulose binding domain;
XX fibre processing; waste paper de-inking; paper pulp; db; gene.
XX
XX Mucor circinelloides.
XX
XX MO200242474-A1.
XX
XX 30-MAY-2002.
XX
XX 21-NOV-2001; 2001MO-JP10188.
XX

```

```

XX 21-NOV-2000; 2000JP-0354296.
PR (MEIJU) MEIJI SEIKA KAISHA LTD.
PA Nakane A, Baba Y, Koga J, Kubota H;
XX WPI: 2002-471729/50.
XX P-PSDB; AAO15055.
XX
XX Cellulose-binding domain-lacking Zymomyces-originated endoglucanase,
XX with effect of endoglucanase activity enhanced in processing fibers,
XX deinking waste paper and improving freeness of paper pulp -
XX Disclosure; Page 70-73; 109pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of
XX Zymomyces-originated endoglucanase enzymes lacking the cellulose
XX binding domain. The Zymomyces-originated endoglucanase enzymes of the
XX invention have enhanced endoglucanase activity. The Zymomyces-
XX originated endoglucanase enzymes of the invention are useful for
XX processing fibres, de-inking waste paper and improving the freeness of
XX paper pulp - which is particularly applicable in detergent compositions.
XX The present DNA sequence represents an endoglucanase-related gene
XX sequence of the invention.
XX
XX Sequence 1017 BP; 233 A; 255 C; 236 G; 293 T; 0 other;
XX
XX Query Match 41.1%; Score 417.6; DB 24; Length 1017;
XX Best Local Similarity 67.8%; Pred. No. 1.2e-116;
XX Matches 655; Conservative 0; Mismatches 284; Indels 27; Gaps 4;
XX
OY 67 GCTGCTGATGATGCAATTTGATGCTCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126
DB 64 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 123
OY 127 TGTGGAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 124 TGTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
OY 181 CTTCCCTGGAAGAGTGGCAATTAATCTTGAAGTGTCTGACAGAGAGC----- 233
DB 184 CTTCCCGATCCACAGTAAATGCTGTAACGCTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 243
OY 234 --TACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291
DB 244 AAGACATCTACTACCAACCGCCCAAGGCTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCT 303
OY 292 CCGGCTAAGAGACTACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351
DB 304 ACACTACCAAGACAATCAAGACTACGACCTGCGGCTTCTAAGCTCTAGCTCTAGC 363
OY 352 TCCAGCGGCAATATTCGCGCTGCTCTGAGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 411
DB 364 TCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
OY 412 TATTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
DB 424 TATTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
OY 472 GTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
DB 484 GTTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
OY 532 TGTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
DB 541 TGTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
OY 592 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
DB 601 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
OY 652 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 711

```


CC invention have enhanced endoglucanase activity. The xygomycetes-
 CC originated endoglucanase enzymes of the invention are useful for
 CC processing fibres, de-inking waste paper and improving the freeness of
 CC paper pulp - which is particularly applicable in detergent compositions.
 CC The present DNA sequence represents an endoglucanase-related gene
 CC sequence of the invention.

XX Sequence 1041 BP; 225 A; 352 C; 248 G; 216 T; 0 other;

Query Match / 29.9%; Score 304.2; DB 24; Length 1041;
 Best Local Similarity 59.9%; Pred. No. 4.4e-82;
 Matches 616; Conservative 0; Mismatches 353; Indels 60; Gaps 4;

```

QY 37 GCTCTGCGCTCGGTACTGAAATGGCTCTGCTGGAATGTGCAATTTGTGCA 96
DB 25 GCCCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 84
QY 97 TGTGTGTGTAAGATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 153
DB 85 TGTGTGTGTAAGATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 144
QY 154 ---GTAAGCAAGATTACTTCTCAATGTTCTTCTGGAAGCAGTGCATTAATCT 210
DB 145 GCCGAAACAAAGAGTGTACTCTCAGTGTATCCCAAGATCAAGTCCAGGCTAACCCC 204
QY 211 TCTGAAAGTCTCACAAGAACTACCACTGCTGCTCACAAGAACTACCACTGCTGCT 270
DB 205 AAGACCACCAACCAACCAACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 264
QY 271 CATAAA-----AAGACTACACT 288
DB 265 ACCAAGGCCACCAACCAACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324
QY 289 GCTCTGCTGTAAGATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 348
DB 325 ACTACCAACCAACCAACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
QY 349 AGCTCAGGCGCAATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408
DB 385 TCTTCCAAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 444
QY 409 CGTTATTTGGAATGCTGTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
DB 445 CGTACTGGGATTTGCTGCAAGCCCTTGTGGCTGGAAGGAAAGCTTCTGTAATGAG 504
QY 469 CCTGTCAATGCTGTAACAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
DB 505 CCTGTATGTCACCTGCTGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561
QY 529 GGCTGTAAAGGTGTAAGATGTAATGTAAGCAACCACTGCTGTAAGCAAG 588
DB 562 GGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621
QY 589 AACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
DB 622 GACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
QY 649 TGTCTTGTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
DB 682 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741
QY 709 CAAGTCACTAAACAGTGTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 768
DB 742 CAGGTCACTAAACAGTGTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 792
QY 769 ATGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
DB 793 ATGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 852
QY 829 GACGCTTGGGCTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
DB 853 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912

```

```

QY 889 TCCGACCTCAAGCTGTTGTAATGAGATTCACTGCTGCAAGACCGTGATACCA 948
DB 913 ACCCAGTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
QY 949 ACCAGTACTTACAGGAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
DB 973 GAGTCACCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
QY 1009 AGAAATTA 1017
DB 1033 CGCAAGTAA 1041

```

RESULT 15

AA014857
 ID AA014857 standard; DNA; 1473 BP.

AC AA014857;

DT 18-FEB-1992 (first entry)

DE Fusarium oxysporum DSM 2672 endoglucanase coding sequence.

KW cellulase; cellulose; ss.

OS Fusarium oxysporum.

PH Key Location/Qualifiers

FT CDS 97..127

PN MO9117243-A.

PD 14-NOV-1991.

PF 08-MAY-1991; 91WO-DK00123.

PR 22-APR-1991; 91DK-0000736.

PR 09-MAY-1990; 90DK-0001159.

XX (NOVO) NOVO NORDISK A/S.

XX Rasmussen G, Mikkelsen JM, Schulein M, Patkar SA, Hagen F;

XX Hjort CM, Hastrup S;

XX WPI; 1991-353765/48.

XX P-PSDB; AAR15272.

XX Cellulase prep. comprising endoglucanase enzyme - used in

XX detergents for cellulose-contg. fabrics or to improve drainage of

XX paper pulp

XX Claim 11; Page 52; 67p; English.

XX The cellulase (i.e. endoglucanase) gene was isolated from a

XX F.oxysporum cDNA library by screening with probes based on the

XX H. insolens 43kD endoglucanase sequence. Positive clones were

XX CC subcloned to PCR amplification using 43kD-specific oligonucleotides

XX CC as primers. The amplified DNA was sequenced.

XX See also AA014856.

XX

Sequence 1473 BP; 343 A; 453 C; 337 G; 340 T; 0 other;

Query Match 18.6%; Score 189.4; DB 12; Length 1473;
 Best Local Similarity 59.0%; Pred. No. 5e-47;
 Matches 369; Conservative 0; Mismatches 241; Indels 15; Gaps 2;

```

QY 380 GTGGTCCCTCTGTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
DB 143 GTGGTCCCTCTGTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 202
QY 440 GTGGTCCCTCTGTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499

```

Db 203 CTGAGCGGAAAGCTGCTGCACGCCCCCTGCTTTAACTTGATAGAAAGCAACC 262
QY 500 CTGCCCTTAGTAGACAGCAATGCCCAAGTGGCTGTAAAGGTGTAAAGTTACATGTGA 559
Db 263 CCAATTCCACACCAATGCTGTACACGGTTGTAGAGGTGTGTCTGTATAGCTTGCA 322
QY 560 ACAGACAACCAACCTTGGCTGTAAACGACAACTTGCCTATAGTTTGGCTGTGCGCA 619
Db 323 CCAACTACTCTCCCTGGGCTGTCAACGATGAGCTTGCTACGAGTTTGGCTACCAAGA 382
QY 620 TCAGTGTGTGTGTGATCTGCGTGTGTGTCTTGTGTTGAACTTACCTTCACTTCTA 679
Db 383 TCTCCGGTGGCTCGAGGCCAGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 442
QY 680 CCTGT 739
Db 443 GCCCGGTCAAGGGGCAAGATGATGTCCAGTCCACACACTGGAGGTGATCTCGGCG 502
QY 740 CCTCTACTGTGTCTCACTTTGACTTGTGCAATGCCCGGTGTGTGTGTGTGTGTGTGT 799
Db 503 ACA-----ACCACTTCGATCTCATGATGCCCGGGGTGTGTGTGTGTGTGTGTGTGT 553
QY 800 GTTGTTCAGGCCAATGGGGTGTCTCCATGACGGTTGGGCTCAAGATACGATGTATTT 859
Db 554 GCTGCACCTCTGAGTTGG-----CAAGGCTCTGGGGGGTGGCCAGTACGGGGTATCT 607
QY 860 CTTCGATCTGACTGTCTAGTCTTCTTCCTCCGCACTCCAGCTGTGTGTGTGTGTGTGT 919
Db 608 CCTCCGAGGGAATGTATGTATGATACCCCGAGCTTCTCAAGACGATGTGCCACTGGGAT 667
QY 920 TCACTGTGTCAAGACGCTGTATACCCAGCATGACTTACAGAGATTAAGTCTGTCTA 979
Db 668 TCGACTGTGTGAGACGCGACCAACCTTGACTTCACTTTGACAGGTTCAAGTCCCA 727
QY 980 AGAATCACCAGCAAGACAGTTG 1004
Db 728 AGGCTCTCTGACATCAGTGAATG 752

Search completed: June 17, 2003, 11:48:55
Job time : 226.839 secs